

DNA Seg Search Summary

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 01:23:19 ; Search time 13662 Seconds
(without alignments)
17851.084 Million cell updates/sec

Title: US-09-775-938A-37

Perfect score: 8380

Sequence: 1 gcaccgttggAACGTTATGG.....arargggcaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:

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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	8196.8	97.8	8380	6	AX083257 Sequence
	2	236.2	2.8	13614	1	Z14098 B.subtilis
	3	236.2	2.8	33615	1	U11039 Bacillus su
	4	236.2	2.8	233780	1	Z99113 Bacillus su
c	5	199.4	2.4	11856	1	AE004344 Vibrio ch
	6	174.8	2.1	1803	1	X54201 P.aerugino
	7	174.8	2.1	10541	1	AE004629 Pseudomon
c	8	169	2.0	342800	1	AP003598 Nostoc sp
	9	167.4	2.0	1805	1	X89712 Anabaena PC
	10	160.2	1.9	7178	1	AJ006977 Myxococcu
c	11	158.4	1.9	11714	1	AE009538 Brucella
	12	139.4	1.7	7735	1	Z35133 B.subtilis
	13	132.4	1.6	2029	6	A43677 Sequence 2
	14	132.4	1.6	2063	8	X60373 P.sativum m
	15	129.2	1.5	2211	8	X76293 N.tabacum g
	16	128.4	1.5	1995	8	AF019907 Vitis vin
	17	126.8	1.5	6000	6	AX083249 Sequence
	18	126.4	1.5	5482	1	U19883 Burkholderi
	19	125.4	1.5	2081	8	L11632 Soybean glu
	20	125.4	1.5	2672	6	AX083254 Sequence
	21	124.6	1.5	4684	6	AX416809 Sequence
c	22	124.2	1.5	348527	1	AP003360 Staphyloc
	23	123.4	1.5	270050	1	AL591977 Listeria
	24	123	1.5	2042	8	AF109694 Brassica
c	25	122.6	1.5	290150	1	AP004824 Staphyloc
	26	122	1.5	1968	8	AF349449 Brassica
	27	121.2	1.4	1993	8	D14049 Arabidopsis
	28	121.2	1.4	2045	8	AY054677 Arabidops
c	29	121	1.4	52276	1	AE014141 Streptoco
c	30	116.6	1.4	12575	1	AE009977 Streptoco
c	31	116.6	1.4	12578	1	AE006497 Streptoco
c	32	114.6	1.4	224650	1	AL596164 Listeria
c	33	114.6	1.4	349980	6	AX417038 Sequence

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 01:20:14 ; Search time 1017 Seconds
(without alignments)
18556.289 Million cell updates/sec

Title: US-09-775-938A-37

Perfect score: 8380

Sequence: 1 gcaccgttggAACGTTATGG.....arargggcaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB ID		
	1	8196.8	97.8	8380	24	AAD29007	Bugula neritina co
	2	5427.8	64.8	5814	24	AAD29008	B. neritina cosmid
	3	160.2	1.9	7178	21	AAA59145	DNA encoding a pep
	4	132.4	1.6	2029	16	AAQ87912	Glutathione-reduct
	5	126.8	1.5	6000	24	AAD28999	Bugula neritina PK
	6	125.4	1.5	2672	24	AAD29004	Bugula neritina co
	7	124.6	1.5	4684	24	ABQ70987	Listeria monocytog
c	8	116.6	1.4	714	24	ABN68868	Streptococcus poly
	9	110.6	1.3	31063	22	AAF28533	Genomic fragment #
c	10	110.2	1.3	3803	22	AAH54197	S. epidermidis gen
c	11	109.4	1.3	4017	22	AAH54064	S. epidermidis gen
	12	108.8	1.3	1359	24	ABN66981	Streptococcus poly
	13	108.2	1.3	7147	19	AAV52156	Streptococcus pneu
c	14	106.6	1.3	726	24	ABN93298	Staphylococcus epi
c	15	106.6	1.3	771	24	ABN68867	Streptococcus poly
	16	106.6	1.3	2155561	24	ABN71527	Streptococcus poly
c	17	105.4	1.3	2944528	24	ABA03041	Listeria monocytog
c	18	105.2	1.3	714	24	ABN71086	Streptococcus poly
	19	105	1.3	5686	24	AAD29001	Bugula neritina co
c	20	104	1.2	717	22	AAH53866	S. epidermidis ope
c	21	104	1.2	717	22	AAH53879	S. epidermidis ope
	22	102.2	1.2	1680	24	ABQ70472	Listeria monocytog
	23	101.8	1.2	7989	20	AAX13206	Enterococcus faeca
c	24	98.2	1.2	717	21	AAA95485	E. coli essential
c	25	98.2	1.2	717	21	AAA88712	E. coli FUN essent
c	26	98.2	1.2	717	22	AAH81406	Escherichia coli p
	27	96.6	1.2	1347	24	ABN66980	Streptococcus poly
	28	94.2	1.1	1350	21	AAA05870	Group B Streptococ
	29	94.2	1.1	1350	22	AAS07028	DNA encoding Group
	30	92.8	1.1	1368	22	AAF94383	Haemophilus influe
	31	92.8	1.1	1368	24	ABK64947	DNA encoding Haemo
c	32	86.6	1.0	654	22	AAS07042	DNA encoding Group
	33	86.6	1.0	2206	22	AAS41779	Genomic sequence #
	34	86.6	1.0	2206	22	AAS41823	Genomic sequence #
	35	86.6	1.0	2206	22	AAS41872	Genomic sequence #
	36	86.6	1.0	2206	22	AAL02886	Human reproductive
	37	86.6	1.0	2206	22	AAL02916	Human reproductive
	38	86.6	1.0	2206	22	AAK69626	Human immune/haema
	39	86.6	1.0	2206	22	AAK85452	Human immune/haema
	40	86.6	1.0	2206	22	AAK85502	Human immune/haema
	41	82.6	1.0	6373	21	AAA51639	pGM795 containing
	42	81.8	1.0	5890	21	AAA51637	Plasmid pGM769 con
	43	81.6	1.0	862	24	AAD29379	Beta-lactamase gen
	44	81.6	1.0	4811	23	AAS92120	DNA encoding novel
	45	81.6	1.0	6062	13	AAQ20765	pAD-CMV19. AAQ20

ALIGNMENTS

RESULT 1

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:32:09 ; Search time 166 Seconds
(without alignments)
15481.634 Million cell updates/sec

Title: US-09-775-938A-37

Perfect score: 8380

Sequence: 1 gcaccgttggAACGTTATGG.....arargggcaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
No.	Score	Match	Length	DB	ID		
<hr/>							
1	108.2	1.3	7147	4	US-08-961-527-23		Sequence 23, Appl
c	2	106.6	1.3	726	4	US-09-134-001C-2761	Sequence 2761, Ap
c	3	80	1.0	1106	1	US-08-041-648-4	Sequence 4, Appli
c	4	80	1.0	1106	1	US-08-041-648-6	Sequence 6, Appli
c	5	80	1.0	1106	1	US-08-041-648-8	Sequence 8, Appli
	6	80	1.0	1163	4	US-09-025-769B-284	Sequence 284, App
c	7	80	1.0	1289	4	US-09-025-769B-361	Sequence 361, App
	8	80	1.0	1947	4	US-09-025-769B-264	Sequence 264, App
	9	80	1.0	2422	1	US-07-867-106-5	Sequence 5, Appli
c	10	80	1.0	2728	4	US-09-025-769B-299	Sequence 299, App
c	11	80	1.0	2755	2	US-07-916-098A-7	Sequence 7, Appli
c	12	80	1.0	2927	2	US-08-941-647A-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:35:14 ; Search time 230 Seconds
(without alignments)
16035.070 Million cell updates/sec

Title: US-09-775-938A-37

Perfect score: 8380

Sequence: 1 gcaccgttggAACGTTATGG.....arargggcaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description	
	No.	Score	Match	Length	DB ID	
<hr/>						
1	8196.8	97.8	8380	10	US-09-775-938A-37	Sequence 37, Appl
2	126.8	1.5	6000	10	US-09-775-938A-29	Sequence 29, Appl
3	125.4	1.5	2672	10	US-09-775-938A-34	Sequence 34, Appl
4	121.2	1.4	1698	9	US-09-938-842A-1742	Sequence 1742, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:29:49 ; Search time 6839 Seconds
(without alignments)
19844.740 Million cell updates/sec

Title: US-09-775-938A-37

Perfect score: 8380

Sequence: 1 gcaccgttggAACGTTATGG.....arargggcaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query			Description
			Match	Length	DB	
	1	114.6	1.4	775	13	BI925816 BI925816 EST545705
	2	114	1.4	612	13	BJ481803 BJ481803
c	3	109.4	1.3	2553	17	BH771010 BH771010 LLMGtag73
	4	104.2	1.2	694	13	BI923097 BI923097 EST543001
	5	103.4	1.2	756	13	BI926373 BI926373 EST546262
	6	99.8	1.2	626	12	BF597723 BF597723 su99e02.y
	7	99.8	1.2	631	10	AW201729 AW201729 sf06e10.y
	8	99.2	1.2	660	10	AW692989 AW692989 NF058A04S
	9	98.6	1.2	720	10	BE038718 BE038718 AB04E07 A
	10	98.2	1.2	543	12	BE800059 BE800059 sq81f09.y
	11	97	1.2	593	10	AW759724 AW759724 sl47b10.y
	12	95.8	1.1	588	13	BI921333 BI921333 EST541236
	13	94.4	1.1	581	10	AV937628 AV937628 AV937628
	14	93.6	1.1	509	14	BQ490169 BQ490169 04-E9435-
c	15	93.2	1.1	888	13	BI684711 BI684711 603307057
	16	92.6	1.1	713	10	BE435454 BE435454 EST406532
	17	88.8	1.1	935	12	BG838279 BG838279 Gc01_10e0
c	18	86.6	1.0	535	17	AZ049308 AZ049308 GSSBru086
c	19	86.6	1.0	773	13	BI686035 BI686035 603313001
	20	86.2	1.0	1931	11	AY103791 AY103791 Zea mays
	21	86	1.0	473	13	BM093562 BM093562 saj10g05.
	22	85.4	1.0	707	9	AU056093 AU056093 AU056093
c	23	83.6	1.0	911	13	BG923556 BG923556 602823195
c	24	83.2	1.0	832	13	BG923768 BG923768 602825893
c	25	83.2	1.0	855	13	BI664231 BI664231 603289174
	26	82	1.0	490	13	BM323249 BM323249 PIC1_17_B
	27	82	1.0	683	14	BQ283215 BQ283215 WHE3087_E
	28	80	1.0	444	14	BQ469551 BQ469551 HZ01C07r
	29	80	1.0	499	10	AV612734 AV612734 AV612734
c	30	80	1.0	575	17	AZ918759 AZ918759 1006006H0
c	31	80	1.0	604	17	AG002706 AG002706 Homo sapi
c	32	80	1.0	711	17	AG010947 AG010947 Homo sapi
c	33	80	1.0	754	13	BG920379 BG920379 602826032
	34	80	1.0	780	14	BQ825693 BQ825693 1030129B0
	35	80	1.0	841	9	AL042026 AL042026 DKFZp434E
c	36	79.8	1.0	803	13	BI149831 BI149831 602849105
	37	79.6	0.9	583	10	BE498405 BE498405 WHE0952_A
	38	79.6	0.9	647	17	AG008943 AG008943 Homo sapi
	39	79.2	0.9	608	13	BM325129 BM325129 PIC1_40_D
c	40	79.2	0.9	872	13	BI855537 BI855537 603382628
	41	78.8	0.9	549	13	BI944287 BI944287 saa09g07.
	42	78.8	0.9	618	14	BQ820772 BQ820772 1030087B0
	43	78	0.9	415	13	BI972926 BI972926 sai84h06.
c	44	78	0.9	801	10	BE569687 BE569687 601332450
	45	77.8	0.9	691	14	BU002083 BU002083 QGG30C17.

ALIGNMENTS